

CLAIMS

1. Peptide comprising essentially the peptide sequence of formula (I),

5 Xaa-Cys-Xab-Cys-Xac-Cys-Xad-Cys-Xae-Cys-Xaf-Cys-Xag
(I)

in which:

Xaa is -NH₂ or a peptide residue comprising
10 from 1 to 10 amino acids, preferably from 1 to 6 amino acids,

Xab is a peptide residue comprising from 1 to 10 amino acids, preferably 10,

Xac is a peptide residue of 3 amino acids,

15 Xad is a peptide residue comprising from 1 to 9 amino acids, preferably 9,

Xae is a peptide residue comprising from 1 to 7 amino acids, preferably 7,

Xaf is a peptide residue of 1 amino acid, and

20 Xag is -OH or a peptide residue comprising from 1 to 5 amino acids, preferably 1 or 2 amino acids.

2. Peptide according to claim 1, characterized in that
Xaa comprises at least one basic amino acid, and/or
25 Xad comprises at least one basic amino acid.

3. Peptide according to claim 2, characterized in that Xad comprises 1, 2, 3 or 4 basic amino acids.

claim 2
 4. Peptide according to ~~either of claims 2~~
 5 *A* ~~and 3~~, characterized in that the basic amino acids are chosen from lysine, arginine or homoarginine.

claim 1
 5. Peptide according to ~~one of claims 1 to~~
 10 *A* ~~4~~, characterized in that Xad represents the following peptide sequence -Lys-Xad'-Xad"-Gly-His-, in which Xad' represents a peptide residue of 1 basic amino acid and Xad" represents a peptide residue comprising from 0 to 5 amino acids, preferably 5.

claim 1
 6. Peptide according to ~~one of claims 1 to~~
 15 *A* ~~5~~, characterized in that Xad represents the following peptide sequence -Lys-Arg-Arg-Gly-Tyr-Lys-Gly-Gly-His-.

7. Peptide according to one of claims 1 to 6, characterized in that Xac comprises at least one acidic amino acid, preferably 1.

claim 1
 8. Peptide according to ~~one of claims 1 to~~
 20 *A* ~~7~~, characterized in that Xac represents the following peptide sequence -Asn-Xac'-Xac"-, in which Xac' represents a peptide residue of 1 amino acid, and Xac" represents a peptide residue of 1 acidic amino acid.

claim 7
 9. Peptide according to ~~either of claims 7~~
 25 *A* ~~and 8~~, characterized in that the acidic amino acids are chosen from glutamic acid (Glu) or aspartic acid (Asp).

10. Peptide according to ^{claim 1} ~~one of claims 1 to 10~~, characterized in that Xac represents the following peptide sequence -Asn-Gly-Glu-.

11. Peptide according to ^{claim 1} ~~one of claims 1 to 10~~, characterized in that

5 Xaa represents the following peptide sequence Xaa'-Gly-Xaa"- in which Xaa' represents NH₂ or a peptide residue comprising 1 to 9 amino acids, preferably 1 to 5 amino acids, and Xaa" represents a peptide residue comprising

10 at least one amino acid, preferably chosen from Leu, Ile, Val, Pro, Ser or Thr, and/or

Xab represents the following peptide sequence -Val-Xab'-Asp-, in which Xab' represents a peptide residue comprising from 0 to 8 amino acids, preferably 8,

15 and/or

Xae represents the following peptide sequence -Gly-Xae'-Asn-, in which Xae' represents a peptide residue comprising from 0 to 5 amino acids, preferably 5, and/or

20 Xaf represents one of the following amino acids Trp, Phe, Leu, Ile or Val and/or

Xag represents the following peptide sequence -Glu-Xag' in which Xag' represents OH or a variable residue having a sequence comprising from 1 to 4 amino acids,

25 preferably 1 amino acid.

12. Peptide according to ^{claim 1} ~~one of claims 1 to 11~~, characterized in that

SUBCY)

Xaa represents the following peptide sequence NH₂-Asp-Lys-Leu-Ile-Gly-Ser-, and/or

Xab represents the following peptide sequence -Val-Trp-Gly-Ala-Val-Asn-Tyr-Thr-Ser-Asp-, and/or

5 Xae represents the following peptide sequence -Gly-Ser-Phe-Ala-Asn-Val-Asn-, and/or

Xaf represents the following amino acid -Trp- and/or

Xag represents the following peptide sequence -Glu-Thr-OH.

10 13. Peptide according to ^{claim 1} ~~one of claims 1 to 12~~, characterized in that it is represented by the identifier No. 2 (SEQ ID NO 2).

14. Peptide according to ^{claim 1} ~~one of claims 1 to 13~~, characterized in that it comprises at either of its

15 ends, or at both ends, peptide residues necessary for its expression and targeting in a host organism.

15. Peptide according to ^{claim 1} ~~one of claims 1 to 14~~, characterized in that the cysteine residues of the peptide of formula (I) form at least one intramolecular

20 disulphide bridge.

16. Peptide according to claim 15, characterized in that it comprises 3 disulphide bridges established between the cysteine residues 1 and 4, 2 and 5, and 3 and 6.

25 17. "Peptide-heliomicine" fusion peptide, characterized in that the heliomicine is a peptide defined according to ^{claim 1} ~~one of claims 1 to 16~~.

SVB CY
Cont

SVB CS

18. Fusion peptide according to claim 17, characterized in that the peptide fused with heliomicine is a signal peptide or a transit peptide.

19. Fusion peptide according to claim 18,
5 characterized in that the transit peptide is the signal peptide of the tobacco PR-1 α gene or the precursor of factor Mat alpha 1 or the signal peptide of the maize polygalacturonase PG1 gene.

20. Fusion peptide according to claim 19,
10 characterized in that it is represented by the sequence identifier No. 1 (SEQ ID NO 1), by the sequence identifier No. 3 (SEQ ID NO 3), or by the sequence identifier No. 18 (SEQ ID NO 18).

21. ~~As~~ As a medicament, the peptide according
15 to one of claims 1 to 20.

22. Composition, characterized in that it comprises the peptide according to ^{claim 1} ~~one of claims 1 to 20~~ and an appropriate vehicle.

23. Nucleic acid fragment, characterized in
20 that it comprises a nucleic acid sequence encoding a peptide according to ^{claim 1} ~~one of claims 1 to 20~~.

24. Nucleic acid fragment according to claim 23, characterized in that it is a nucleotide sequence of the DNA type.

25. Nucleic acid fragment according to claim 24, characterized in that the nucleotide sequence of the DNA type comprises the DNA sequence described by bases 16 to 147 of the sequence identifier No. 1 (SEQ ID NO 1), by the sequence identifier No. 2 (SEQ ID NO 2), by bases 3 to 224 of the sequence identifier No. 3 (SEQ ID NO 3), or by bases 7 to 205 of the sequence identifier No. 18 (SEQ ID NO 18), a homologous sequence or a sequence complementary to the said sequence.

10 26. Chimeric gene comprising a coding sequence as well as heterologous regulatory elements at the 5' and 3' positions capable of functioning in a host organism, in particular plants, characterized in that the coding sequence comprises at least one DNA
15 fragment as defined in claims ~~23 to 25~~.

27. Chimeric gene according to claim 26, characterized in that the host organism is a microorganism.

28. Chimeric gene according to claim 26,
20 characterized in that the host organism is chosen from plant cells and plants.

29. Cloning or expression vector for the transformation of a host organism, characterized in that it comprises at least one replication origin and
25 at least one chimeric gene as defined in claims ~~26 to 28~~.

A 30. Transformed host organisms, characterized in that they contain a nucleic acid fragment according to claims 23 to 25, or a chimeric gene according to claims 26 to 28.

5 31. Transformed host organism according to claim 30, characterized in that it includes microorganisms, plant cells or plants.

32. Transformed host organism according to claim 30, characterized in that it is a plant
10 containing transformed cells.

33. Host organism according to claim 32, characterized in that the plant is regenerated from transformed cells.

15 34. Transformed host organism according to claim 30, characterized in that the microorganism is chosen from bacteria, in particular *E. coli*, yeasts, in particular of the genera *Saccharomyces* or *Kluyveromyces*, *Pichia*, fungi, in particular *Aspergillus*, or baculoviruses.

A 20 35. Transformed plant cell, characterized in that it contains a nucleic acid fragment according to claims 23 to 25 or a chimeric gene according to claims 26 to 28.

25 36. Transformed plant, characterized in that it comprises at least one transformed plant cell according to claim 35.

37. Transformed plant according to claim 36, characterized in that it is resistant to diseases caused by *Cercospora*, in particular *Cercospora beticola*, *Cladosporium*, in particular *Cladosporium herbarum*, *Fusarium*, in particular *Fusarium culmorum* or *Fusarium graminearum*, or by *Phytophthora*, in particular *Phytophthora cinnamomi*.

38. Transformed plant, characterized in that it is derived from the cultivation and/or crossing of the plants according to ^{claim 36} ~~either of claims 36 and 37.~~

39. Seeds of transformed plants according to ^{claim 36} ~~one of claims 36 to 38.~~

40. Method of transforming host organisms, in particular plant cells or plants, characterized in that at least one nucleic acid fragment according to ~~claims 23 to 25 or a chimeric gene according to one of claims 26 to 28~~ is inserted into the said host organism.

41. Method according to claim 40, characterized in that the host organism is a plant cell or a plant.

42. Method according to claim 41, characterized in that a plant is regenerated from the plant cell or from the transformed plant.

A

43. Method of cultivating transformed plants according to ^{claim 36} ~~one of claims 36 to 38~~, characterized in that it consists in planting the seeds of the said transformed plants in a plot of a field appropriate for cultivating the said plants, in applying to the said plot of the said field an agrochemical composition, without substantially affecting the said seeds or the said transformed plants, then in harvesting the cultivated plants when they arrive at the desired maturity and optionally in separating the seeds from the harvested plants.

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44. Method of cultivation according to claim ~~33~~, characterized in that the agrochemical composition comprises at least one active product having at least one fungicidal and/or bactericidal activity.

45. Method of cultivation according to claim 44, characterized in that the active product exhibits an activity which is complementary to that of the peptide according to one of claims 1 to 20.

46. Method of preparing heliomicine defined according to ^{claim 1} ~~one of claims 1 to 20~~, characterized in that it comprises the steps of culturing a transformed organism ^A ~~according to one of claims 30 to 34~~ in an appropriate culture medium, followed by the extraction and total or partial purification of the heliomicine obtained.